CCAGCAGCTG CAAGGTGCAA GAAGAAGAAG ATCCCAGGGA GGAAAATGTG 50
CTGGAGACCC CTGTGTCGG- TTCCTGTGGC TTTGGTCCTA TCTGTCTTAT 100
GTTCAAGCAG TGCCTATCCA GAAAGTCCAG GATGACACCA AAACCCTCAT 150
CAAGACCATT GTCACCAGGA TCAATGACAT TTCACACACG CAGTCGGTAT 200
CCGCCAAGCA GAGGGTCACT GGCTTGGACT TCATTCCTGG GCTTCACCCC 250
ATTCTGAGTT GTTCCAAGAT GGACCAGACT CTGGCAGTCT ATCAACAGGT 300
CCTCACCAGC CTGCCTTCCC AAAATGTGCT GCAGATAGCC AATGACCTGG 350
AGAATCTCCG AGACCTCCTC CATCTGCTGG CCTTCTCCAA GAGCTGCTCC 400
CTGCCTCAGA CCAGTGGCCT GCAGAAGCCA GAGAGCCTGG ATGGCGTCCT 450
GGAAGCCTCA CTCTACTCCA CAGAGGTGGT GGCTTTGAGC AGGCTGCAGG 500
GCTCTCTGCA GGACATTCTT CAACAGTTGG ATGTTAGCCC TGAATGCTGA 550
AGTTTCAAAG GCCAC-CAGG CTCCCAAGAA TCATGTAGAG GGAAGAAACC 600
TTGGCTTCCA GGGGTCTTCA GGA--GAAGA G-AGC-CATG TGCACAC--- 650
ATCCA----T CATTCA-TTT CTCTCCCTCC TGTAGACCAC ----CCAT-- 700
- 701

FIG.1

---G--GTTG	CAAGGCCCAA	GAAGCCCA--	-TCCTGGGAA	GGAAAATGCA	50
TTGGGGAACC	CTGTG-CGGA	TTCTTGTGGC	TTTGGCCCTA	TCTTTTCTAT	100
GTCCAAGCTG	TGCCCATCCA	AAAAGTCCAA	GATGACACCA	AAACCCTCAT	150
CAAGACAATT	GTCACCAGGA	TCAATGACAT	TTCACACACG	CAGTCAGTCT	200
CCTCCAAACA	GAAAGTCACC	GGTTTGGACT	TCATTCCTGG	GCTCCACCCC	250
ATCCTGACCT	TATCCAAGAT	GGACCAGACA	CTGGCAGTCT	ACCAACAGAT	300
CCTCACCAGT	ATGCCTTCCA	GAAACGTGAT	CCAAATATCC	AACGACCTGG	350
AGAACCTCCG	GGATCTTCTT	CACGTGCTGG	CCTTCTCTAA	GAGCTGCCAC	400
TTGCCCTGGG	CCAGTGGCCT	GGAGACCTTG	GACAGCCTGG	GGGGTGTCCT	450
GGAAGCTTCA	GGCTACTCCA	CAGAGGTGGT	GGCCCTGAGC	AGGCTGCAGG	500
GGTCTCTGCA	GGACATGCTG	TGGCAGCTGG	ACCTCAGCCC	TGGGTGCTGA	550
GGCCTTGAAG	GTCACTCTTC	CTGCAAGGAC	T-ACGTTAAG	GGAAGGAACT	600
CTGGTTTCCA	GGTATCTCCA	GGATTGAAGA	GCATTGCATG	GACACCCCTT	650
ATCCAGGACT	CTGTCAATTT	CCCTGACTCC	TCTAAGCCAC	TCTTCCAAAG	700
G					701

FIG.2

1	Met Cys Trp Arg Pro Leu Cys Arg Phe Leu Trp Leu Trp Ser Tyr
16	Leu Ser Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp
31	Thr Lys Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile
46	Ser His Thr Gln Ser Val Ser Ala Lys Gln Arg Val Thr Gly Leu
61	Asp Phe Ile Pro Gly Leu His Pro Ile Leu Ser Leu Ser Lys Met
76	Asp Gln Thr Leu Ala Val Tyr Gln Gln Val Leu Thr Ser Leu Pro
91	Ser Gln Asn Val Leu Gln Ile Ala Asn Asp Leu Glu Asn Leu Arg
106	Asp Leu Leu His Leu Leu Ala Phe Ser Lys Ser Cys Ser Leu Pro
121	Gln Thr Ser Gly Leu Gln Lys Pro Glu Ser Leu Asp Gly Val Leu
136	Glu Ala Ser Leu Tyr Ser Thr Glu Val Val Ala Leu Ser Arg Leu
151	Gln Gly Ser Leu Gln Asp Ile Leu Gln Gln Leu Asp Val Ser Pro
166	Glu Cys End

FIG.3

1 MET HIS TRP GLY THR LEU CYS GLY PHE LEU TRP LEU TRP PRO TYR

16 LEU PHE TYR VAL GLN ALA↓VAL PRO ILE GLN LYS VAL GLN ASP ASP

31 THR LYS THR LEU ILE LYS THR ILE VAL THR ARG ILE ASN ASP ILE

46 SER HIS THR GLN SER VAL SER SER LYS GLN LYS VAL THR GLY LEU

61 ASP PHE ILE PRO GLY LEU HIS PRO ILE LEU THR LEU SER LYS MET

76 ASP GLN THR LEU ALA VAL TYR GLN GLN ILE LEU THR SER MET PRO

91 SER ARG ASN VAL ILE GLN ILE SER ASN ASP LEU GLU ASN LEU ARG

106 ASP LEU LEU HIS VAL LEU ALA PHE SER LYS SER CYS HIS LEU PRO

121 TRP ALA SER GLY LEU GLU THR LEU ASP SER LEU GLY GLY VAL LEU

136 GLU ALA SER GLY TYR SER THR GLU VAL VAL ALA LEU SER ARG LEU

151 GLN GLY SER LEU GLN ASP MET LEU TRP GLN LEU ASP LEU SER PRO

166 GLY CYS END

FIG.4

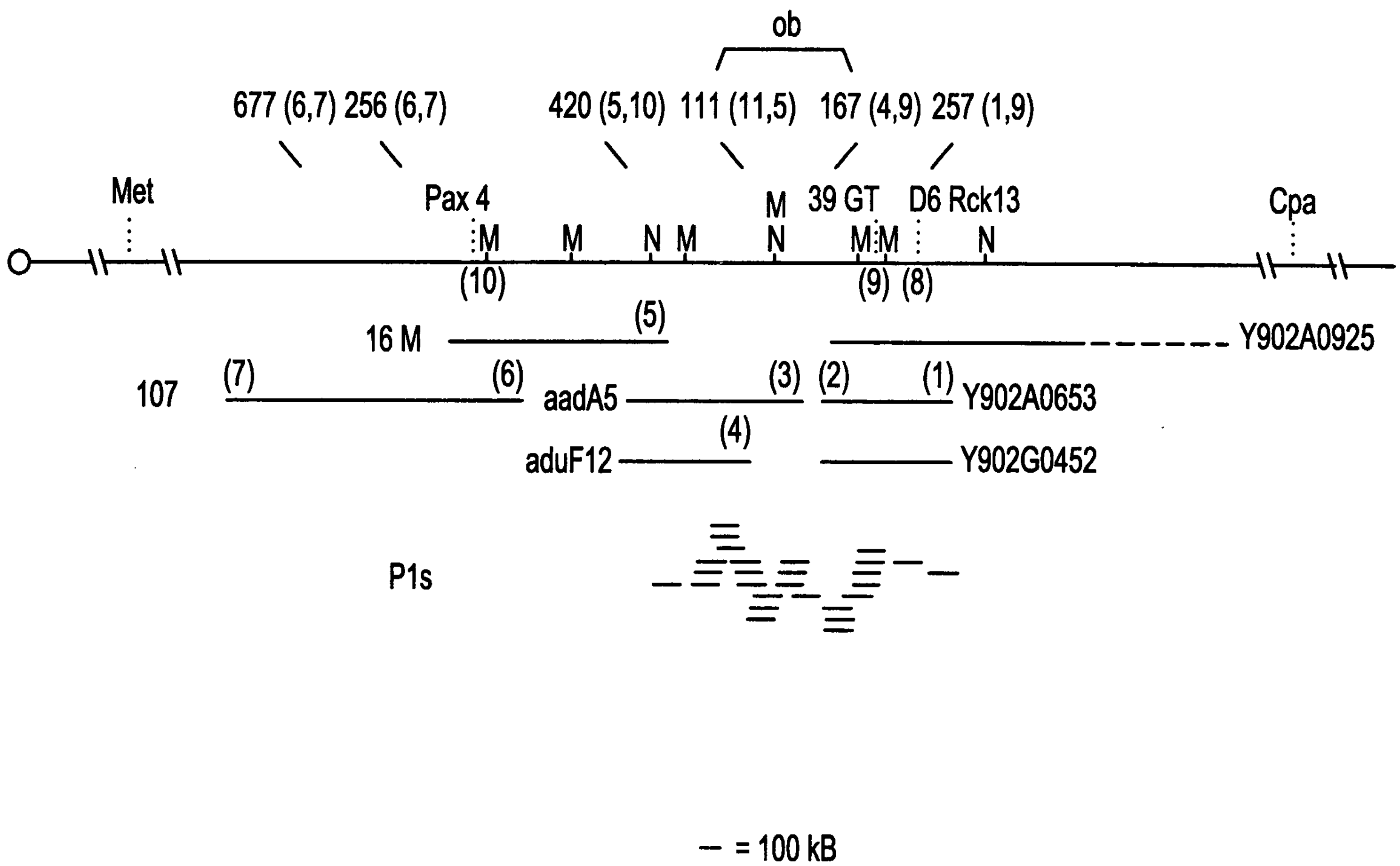
1	Met Cys Trp Arg Pro Leu Cys Arg Phe Leu Trp Leu Trp Ser Tyr
16	Leu Ser Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp
31	Thr Lys Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile
46	Ser His Thr Ser Val Ser Ala Lys Gln Arg Val Thr Gly Leu Asp
61	Phe Ile Pro Gly Leu His Pro Ile Leu Ser Leu Ser Lys Met Asp
76	Gln Thr Leu Ala Val Tyr Gln Gln Val Leu Thr Ser Leu Pro Ser
91	Gln Asn Val Leu Gln Ile Ala Asn Asp Leu Glu Asn Leu Arg Asp
106	Leu Leu His Leu Leu Ala Phe Ser Lys Ser Cys Ser Leu Pro Gln
121	Thr Ser Gly Leu Gln Lys Pro Glu Ser Leu Asp Gly Val Leu Glu
136	Ala Ser Leu Tyr Ser Thr Glu Val Val Ala Leu Ser Arg Leu Gln
151	Gly Ser Leu Gln Asp Ile Leu Gln Gln Leu Asp Val Ser Pro Glu
166	Cys End

FIG.5

1 Met His Trp Gly Thr Leu Cys Gly Phe Leu Trp Leu Trp Pro Tyr
16 Leu Phe Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp
31 Thr Lys Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile
46 Ser His Thr Ser Val Ser Ser Lys Gln Lys Val Thr Gly Leu Asp
61 Phe Ile Pro Gly Leu His Pro Ile Leu Thr Leu Ser Lys Met Asp
76 Gln Thr Leu Ala Val Tyr Gln Gln Ile Leu Thr Ser Met Pro Ser
91 Arg Asn Val Ile Gln Ile Ser Asn Asp Leu Glu Asn Leu Arg Asp
106 Leu Leu His Val Leu Ala Phe Ser Lys Ser Cys His Leu Pro Trp
121 Ala Ser Gly Leu Glu Thr Leu Asp Ser Leu Gly Gly Val Leu Glu
136 Ala Ser Gly Tyr Ser Thr Glu Val Val Ala Leu Ser Arg Leu Gln
151 Gly Ser Leu Gln Asp Met Leu Trp Gln Leu Asp Leu Ser Pro Gly
166 Cys End

FIG.6

FIG. 7



ob
677 (6,7)
256 (6,7)
420 (5,10)
111 (11,5)
167 (4,9)
257 (1,9)
Met
Pax 4
39 GT
D6 Rck13
Cpa
M
M
N
M
M
N
M:M
N
(10)
(9)
(8)
16 M
(5)
Y902A0925
107
(7)
(6)
aadA5
(3)
(2)
(1)
Y902A0653
(4)
aduF12
Y902G0452
P1s
— = 100 kB

FIG. 8

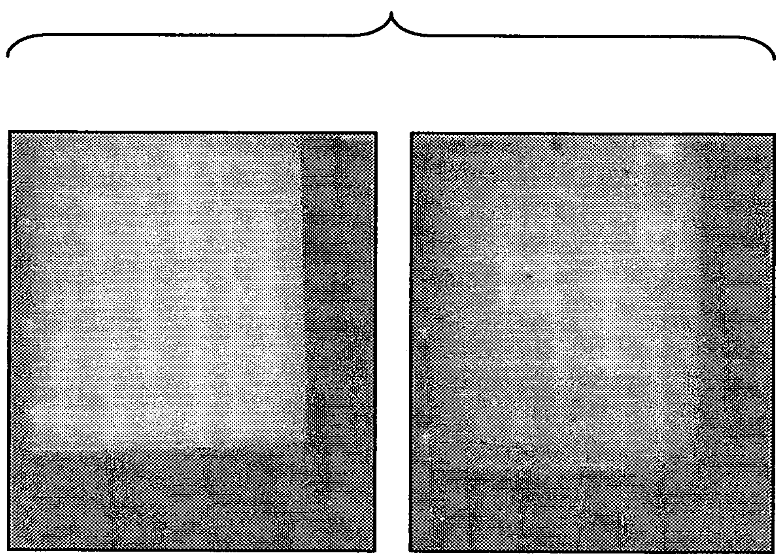
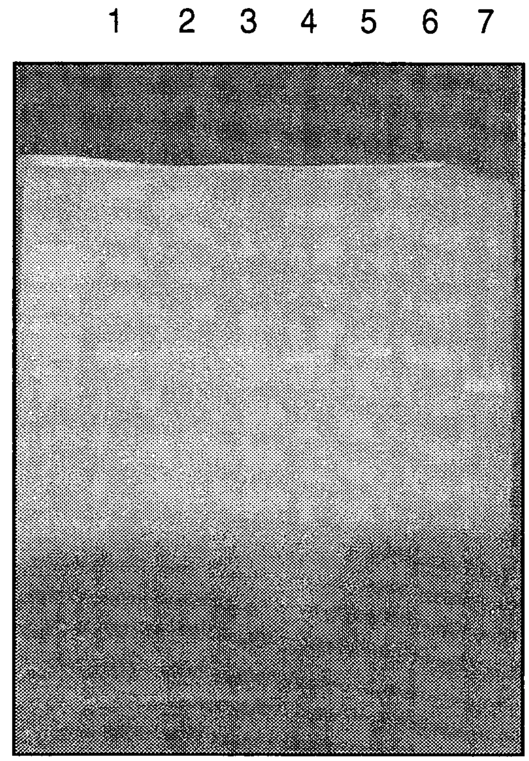


FIG. 9



```
           +10        +20        +30        +40
GTGCAAGAAG AAGAAGATCC CAGGGCAGGA AAATGTGCTG GAGACCCCTG
---------- ---------- ---------- ---------- ----------
CACGTTCTTC TTCTTCTAGG GTCCCGTCCT TTTACACGAC CTCTGGGGAC

           +10        +20        +30        +40
TGTCGGGTCC NGTGGNTTTG GTCCTATCTG TCTTATGTNC AAGCAGTGCC
---------- ?----?---- ---------- --------?- ----------
ACAGCCCAGG NCACCNAAAC CAGGATAGAC AGAATACANG TTCGTCACGG

           +10        +20        +30        +40
TATCCAGAAA GTCCAGGATG ACACCAAAAG CCTCATCAAG ACCATTGTCA
---------- ---------- ---------- ---------- ----------
ATAGGTCTTT CAGGTCCTAC TGTGGTTTTC GGAGTAGTTC TGGTAACAGT

           +10        +20        +30        +40
NCAGGATCAC TGANATTTCA CACACG
?--------- ---?------ ------
NGTCCTAGTG ACTNTAAAGT GTGTGC
```

FIG.10

FIG. 11

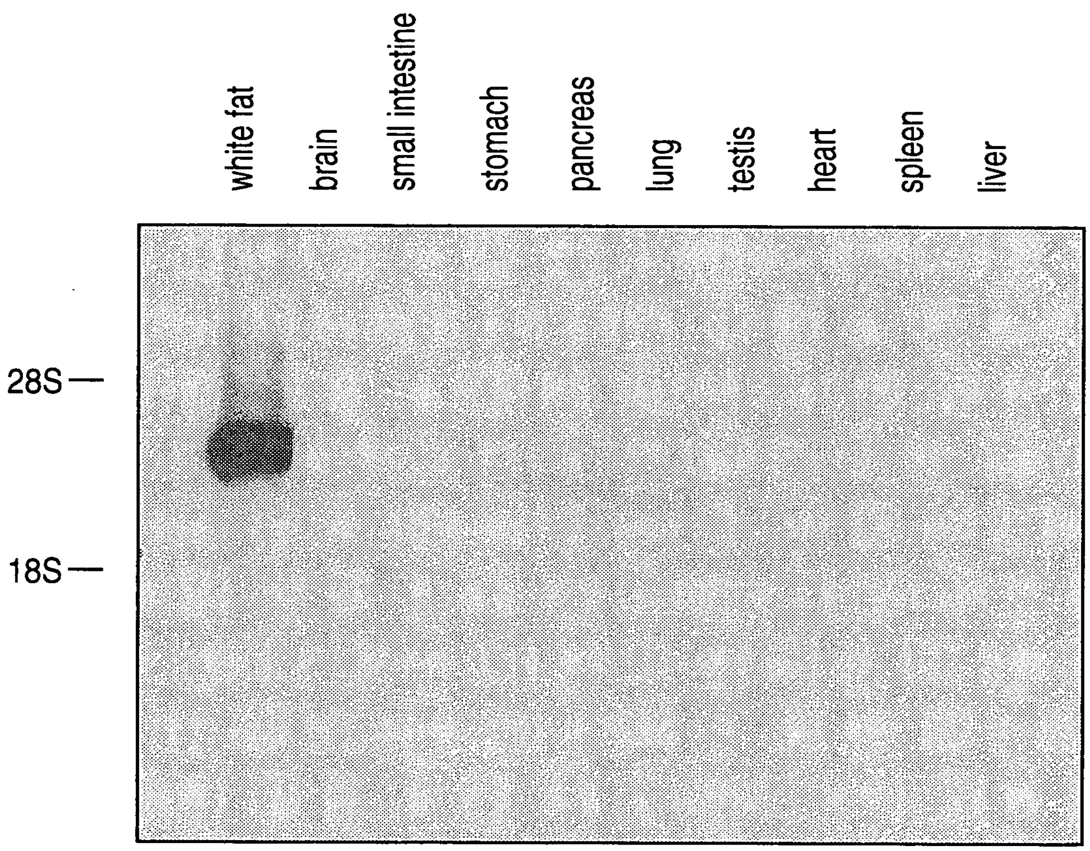

white fat
brain
small intestine
stomach
pancreas
lung
testis
heart
spleen
liver
28S
18S

FIG. 12

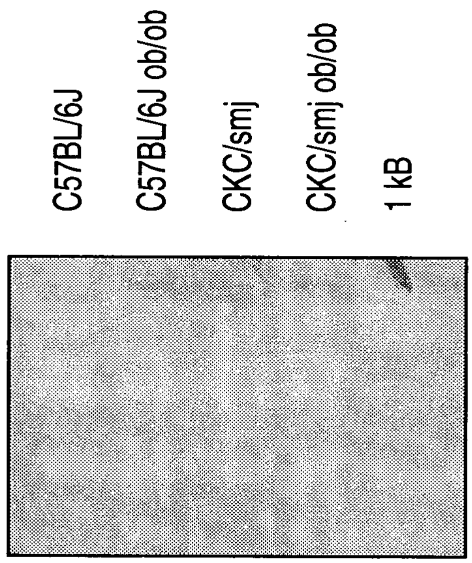
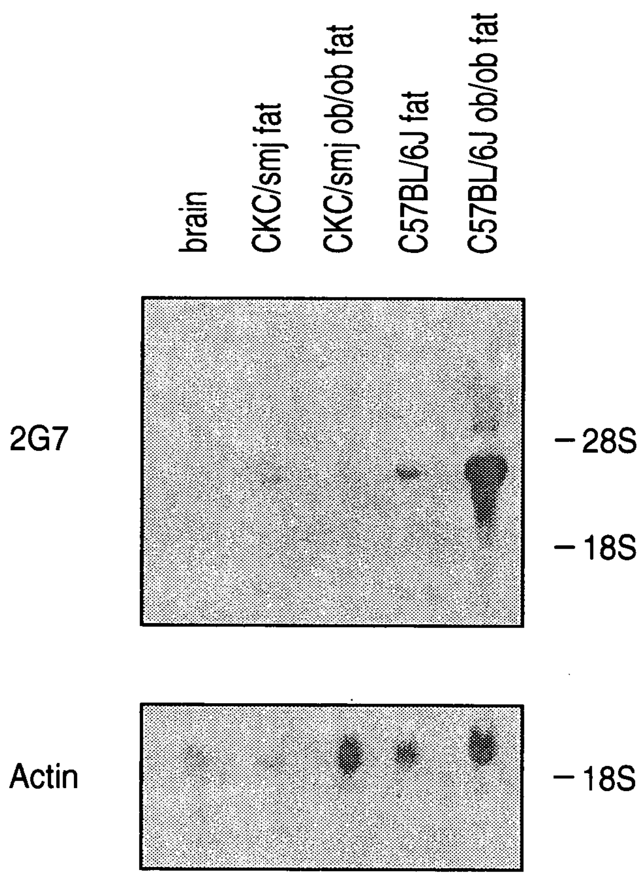
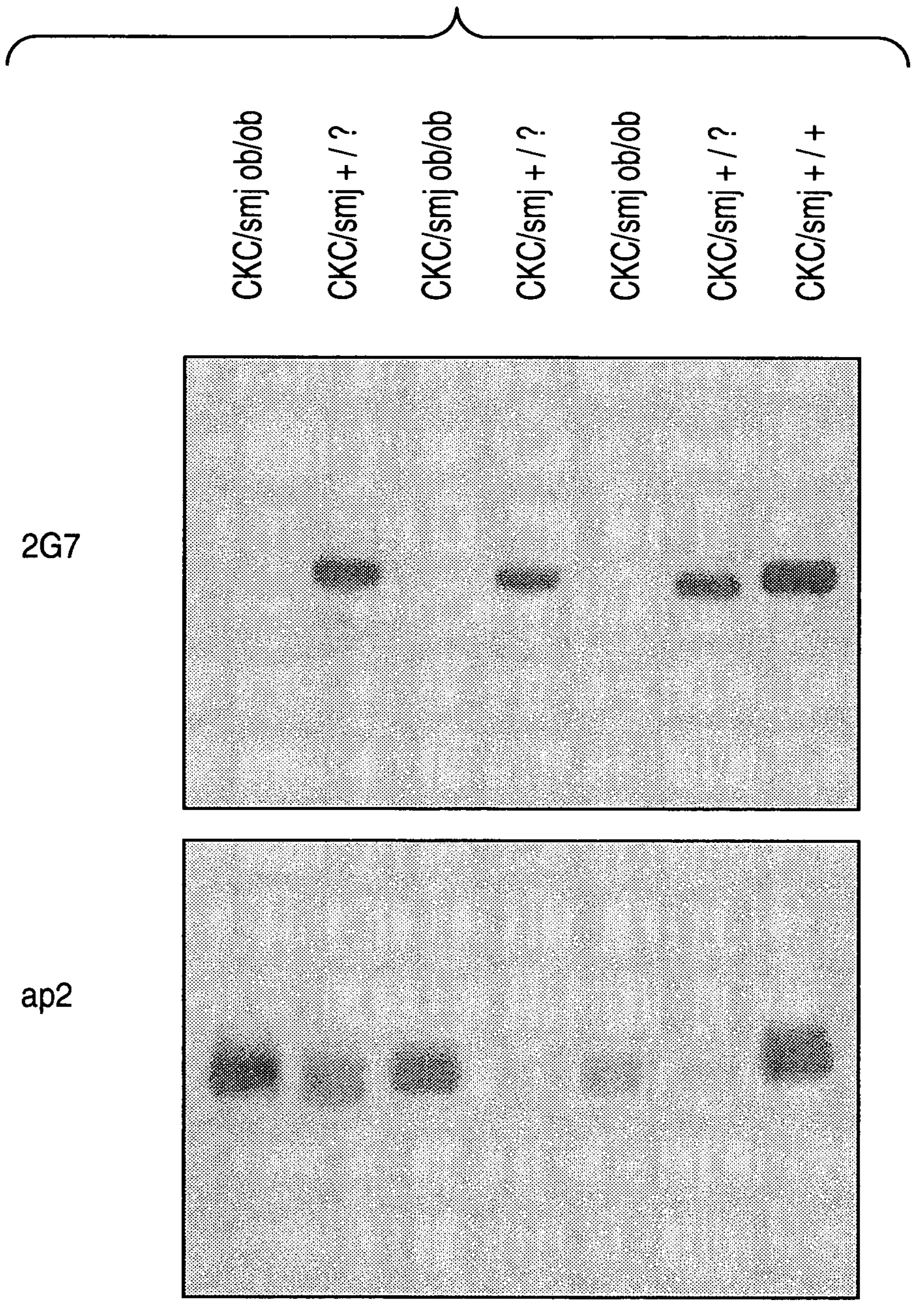


FIG. 13



brain
CKC/smj fat
CKC/smj ob/ob fat
C57BL/6J fat
C57BL/6J ob/ob fat
2G7
– 28S
– 18S
Actin
– 18S

FIG. 14


CKC/smj ob/ob
CKC/smj + / ?
CKC/smj ob/ob
CKC/smj + / ?
CKC/smj ob/ob
CKC/smj + / ?
CKC/smj + / +
2G7
ap2

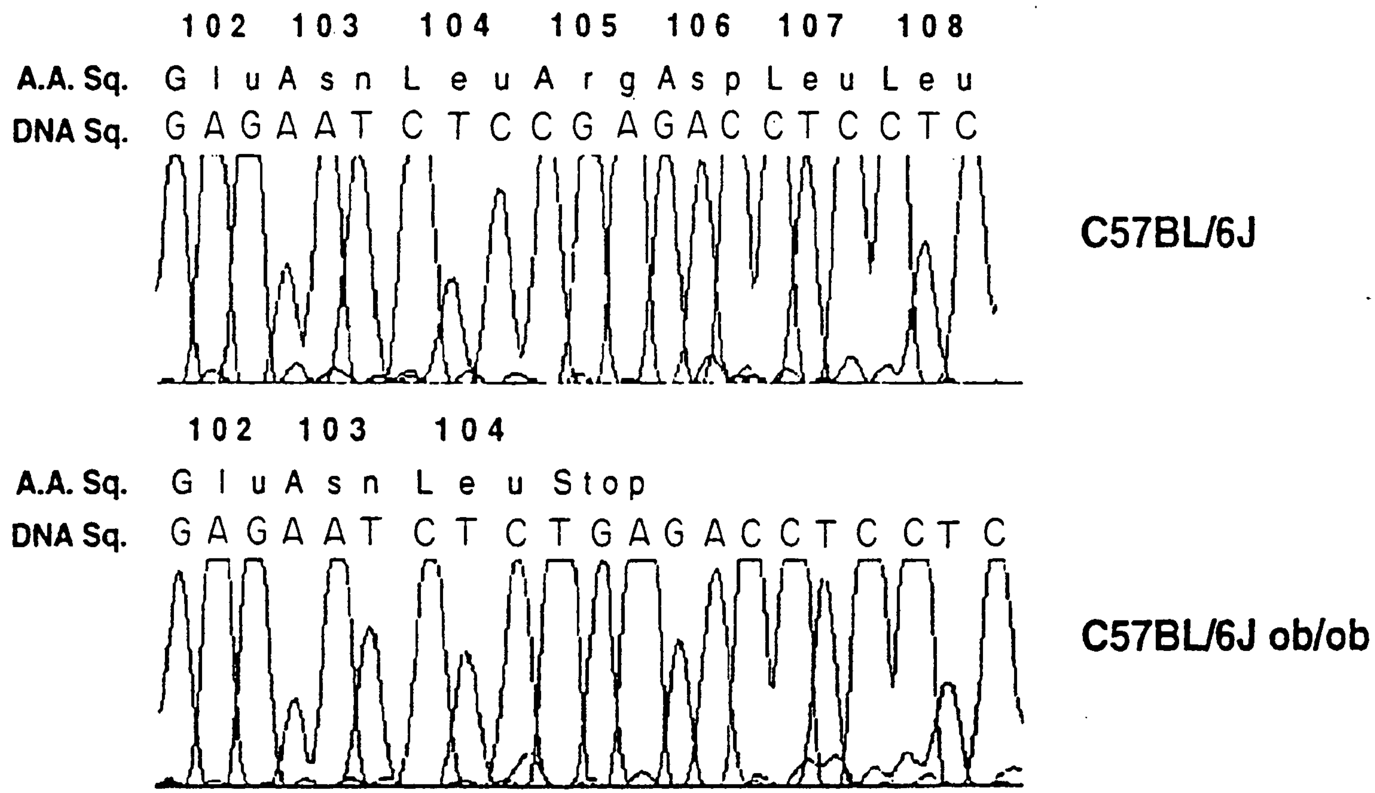
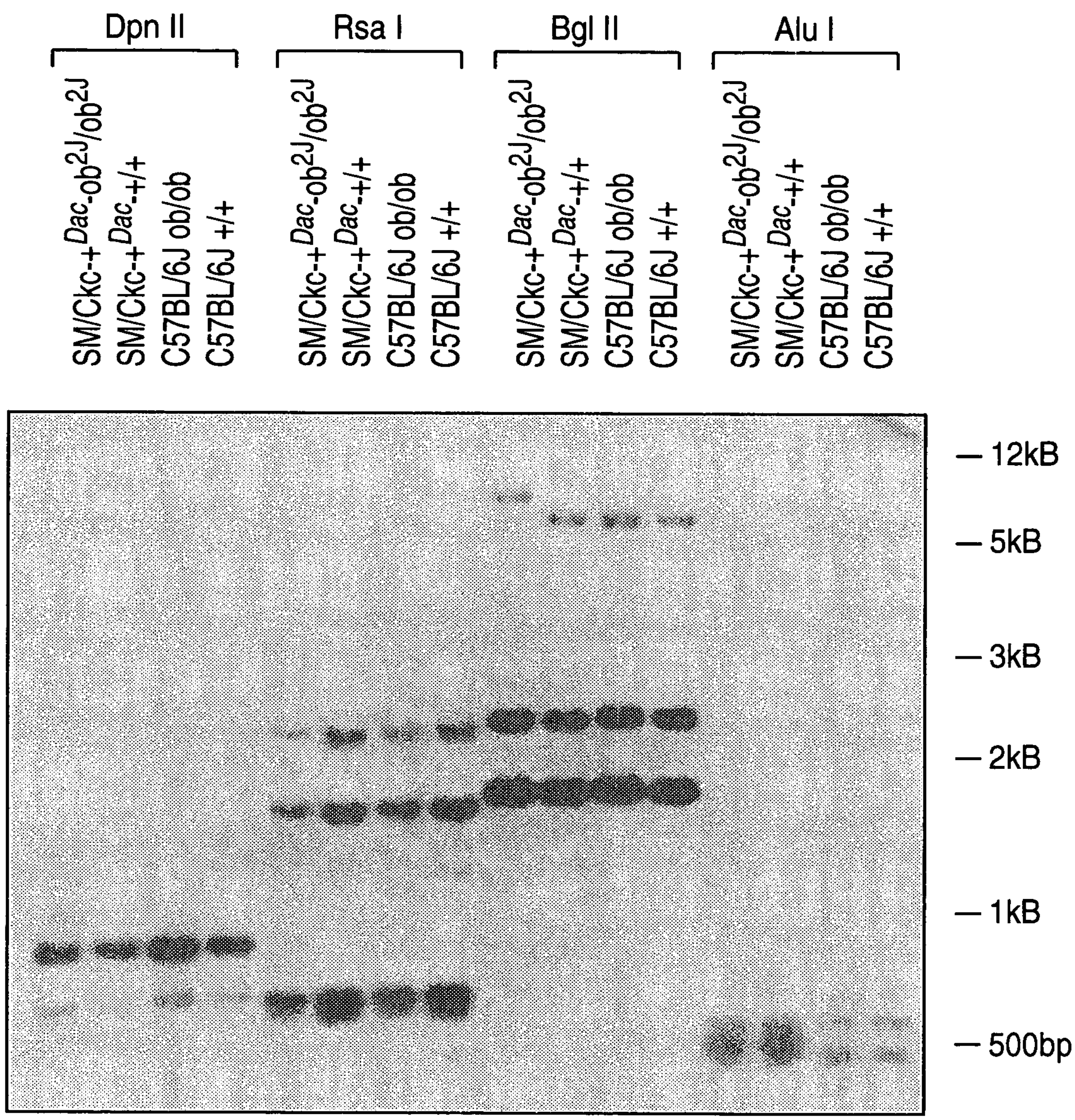

102 103 104 105 106 107 108
A.A. Sq. G l u A s n L e u A r g A s p L e u L e u
DNA Sq. G A G A A T C T C C G A G A C C T C C T C
C57BL/6J
102 103 104
A.A. Sq. G l u A s n L e u Stop
DNA Sq. G A G A A T C T C T G A G A C C T C C T C
C57BL/6J ob/ob

FIG.15

FIG. 16



Dpn II
Rsa I
Bgl II
Alu I
SM/Ckc-$+^{Dac}$-ob^{2J}/ob^{2J}
SM/Ckc-$+^{Dac}$-+/+
C57BL/6J ob/ob
C57BL/6J +/+
12kB
5kB
3kB
2kB
1kB
500bp

FIG. 17

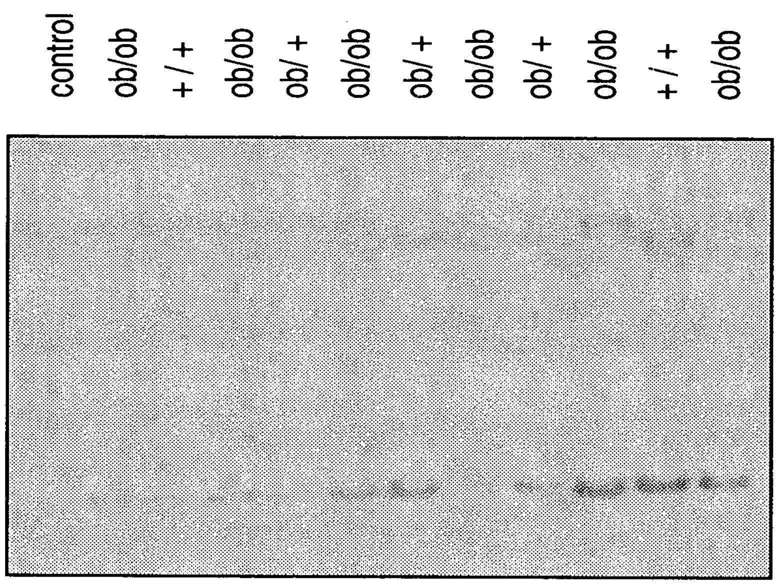
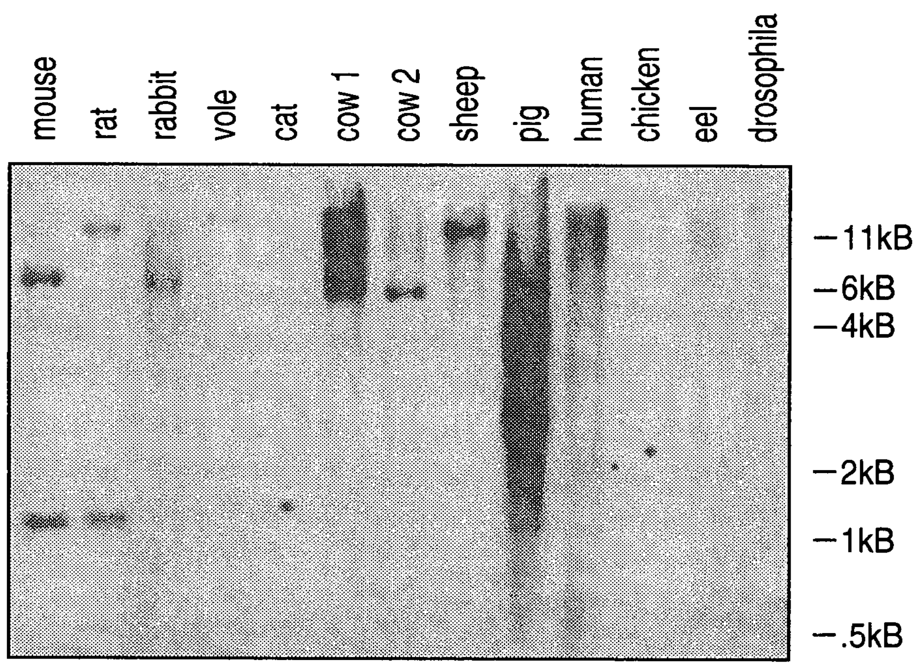


FIG. 18


mouse
rat
rabbit
vole
cat
cow 1
cow 2
sheep
pig
human
chicken
eel
drosophila
11kB
6kB
4kB
2kB
1kB
.5kB

```
                    T7 PROMOTER PRIMER 69348-1
                     ------------------->
                        T7 PROMOTER
 BGLII               ---------------->      LAC OPERATOR       XBAI
AGATCTCGATCCCGCGAAATTAATACGACTCACTATAGGGGAATTGTGAGCGGATAACAATTCCCCTCTACA

                   RBS          NCOI          HIS•TAG
AATAATTTTGTTTAACTTTAAGAAGGAGATATACCATGGGCAGCAGCCATCATCATCATCATCACAGCAGCGGC
                                  MetGlySerSerHisHisHisHisHisHisSerSerGly

                 NDEI   XHOI BAMHI
CTGGTGCCGCGCGGCAGCCATATGCTCGAGGATCCCGCTGCTAACAAAGCCCGAAAGGAAGCTGAGTTGGCT
LeuValProArgGlySerHisMetLeuGluAspProAlaAlaAsnLysAlaArgLysGluAlaGluLeuAla
  THROMBIN

     BPUI1021                       T7 TERMINATOR
GCTGCCACCGCTGAGCAATAACTAGCATAACCCCTTGGGGCCTCTAAACGGGTCTTGAGGGGTTTTTTG
AlaAlaThrAlaGluGlnEnd
    <-----------------------
    T7 TERMINATOR PRIMER #69337-1
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FIG.19